

0598
0321

#2

ENTERED

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/090,455

DATE: 03/19/2002 P.S.
 TIME: 15:56:14

Input Set : A:\406.app
 Output Set: N:\CRF3\03192002\J090455.raw

4 <110> APPLICANT: Chen, Hongyun
 5 Le Bihan, Stephane
 7 <120> TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF
 10 <130> FILE REFERENCE: 100103.406
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/090,455
 13 <141> CURRENT FILING DATE: 2002-03-01
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3455
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1

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 27 aaggtggaga accacatcac tgaagccag cgtttctccc acctgccaa gcgctcagcc 180
 28 gtggacatcg agttcgtgga gctgtcctat tccgtgcggg agggggccctg ctggcgcaaa 240
 29 aggggtttata agacccttct caagtgcctc tcaggtaaatt tctgccgcgg ggagctgatt 300
 30 ggcacatcgg gccctcagg ggtggcaag tctacattca tgaacatctt ggcaggatac 360
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 33 ttggaagcca tgatggtctc tgctaacctg aatcttactg agaatcccg tgtgaaaaac 540
 34 gatctcgtga cagagatcct gacggcactg ggctgatgt cgtgtcccca cagaggaca 600
 35 gccctgctct ctggcgggca gaggaagcgt ctggccatcg ccctggagct ggtcaacaac 660
 36 ccgctgtca tgttctttga tgagcccacc agtgggtctg atagcgctc ttgtttccaa 720
 37 gtgggtgtccc tcatgaagtc cctggcacag gggggccgta ccatcatctg caccatccac 780
 38 cagcccagtg ccaagctctt tgagatgttt gacaagctct acatcctgag ccagggtcag 840
 39 tgcattctca aaggagtggg caccaacctg atcccctatc taaagggact cggcttgcat 900
 40 tgcccacct accacaacct ggctgacttc atcatcgagg tggcctctgg cgagtatgga 960
 41 gacctgaacc ccatgttgtt cagggtctgt cagaatgggc tgtgcgctat ggctgagaag 1020
 42 aagagcagcc ctgagaagaa cgaggctcct gccccatgoc ctcttgtcc tccggaagtg 1080
 43 gatcccattg aaagccacac ctttgccacc agcaccctca cacagttctg catcctcttc 1140
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55 ttccgggagc cacagagcat cctccgagcg ctggatgtgg aggatgccaa gctctacatg 1860
56 gacttcctgg tcttgggcat cttcttcccta gccctgcggc tgctggccta ccttgtgctg 1920
57 cgttaccggg tcaagtccaga gagatagagg cttgccccag cctgtacccc agcccctgca 1980
58 gcagggaagcc cccagtccca gccctttggg actgttttaa ctttatagac ttgggcactg 2040
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61 tcccaagttg atgcggtttg tagcttccctc cctactctct ccaacacctg catgcaaaga 2220
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63 agccctaggg tctctagggc cccacttaca actgaccaa gtggccccct ctgggggtcc 2340
64 ccaccacaca agtgtttgta aactgggctg ctataagggt ggagttccag ggctgggccc 2400
65 tggtggaagtc cactggaagt cccattatgg atgttgaaat ggacagggaa ggactctgga 2460
66 agtctcttcc tccctccctc cttctctcca cccctagacc ctggctgact tggacaatct 2520
67 gccaggacag aagctggggt ttctgtctag gtcaccactc ccaatccctg ggattggaga 2580
68 ggctgggggc tgtgggatgc cccatccccc tccccatcac ctttgggtgg ggagggcct 2640
69 ggtggcacct gtgcaataat gtctgtgttt ctctcccacc tgccactgga actggagaat 2700
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81 ttttccccct ttttccctga cacatccctg tctacctcct ctcacctgc cacagattct 3420
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84 <210> SEQ ID NO: 2

85 <211> LENGTH: 646

86 <212> TYPE: PRT

87 <213> ORGANISM: Homo sapiens

89 <400> SEQUENCE: 2

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91 1 5 10 15
92 Ala Val Ala Met Ala Val Thr Leu Glu Asp Gly Ala Glu Pro Pro Val
93 20 25 30
94 Leu Thr Thr His Leu Lys Lys Val Glu Asn His Ile Thr Glu Ala Gln
95 35 40 45
96 Arg Phe Ser His Leu Pro Lys Arg Ser Ala Val Asp Ile Glu Phe Val
97 50 55 60
98 Glu Leu Ser Tyr Ser Val Arg Glu Gly Pro Cys Trp Arg Lys Arg Gly
99 65 70 75 80
100 Tyr Lys Thr Leu Leu Lys Cys Leu Ser Gly Lys Phe Cys Arg Arg Glu
101 85 90 95
102 Leu Ile Gly Ile Met Gly Pro Ser Gly Ala Gly Lys Ser Thr Phe Met
103 100 105 110
104 Asn Ile Leu Ala Gly Tyr Arg Glu Ser Gly Met Lys Gly Gln Ile Leu
105 115 120 125

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106 Val Asn Gly Arg Pro Arg Glu Leu Arg Thr Phe Arg Lys Met Ser Cys
107      130      135      140
108 Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His Leu Thr Val Leu Glu
109 145      150      155      160
110 Ala Met Met Val Ser Ala Asn Leu Asn Leu Thr Glu Asn Pro Asp Val
111      165      170      175
112 Lys Asn Asp Leu Val Thr Glu Ile Leu Thr Ala Leu Gly Leu Met Ser
113      180      185      190
114 Cys Ser His Thr Arg Thr Ala Leu Leu Ser Gly Gly Gln Arg Lys Arg
115      195      200      205
116 Leu Ala Ile Ala Leu Glu Leu Val Asn Asn Pro Pro Val Met Phe Phe
117      210      215      220
118 Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser Cys Phe Gln Val Val
119 225      230      235      240
120 Ser Leu Met Lys Ser Leu Ala Gln Gly Gly Arg Thr Ile Ile Cys Thr
121      245      250      255
122 Ile His Gln Pro Ser Ala Lys Leu Phe Glu Met Phe Asp Lys Leu Tyr
123      260      265      270
124 Ile Leu Ser Gln Gly Gln Cys Ile Phe Lys Gly Val Val Thr Asn Leu
125      275      280      285
126 Ile Pro Tyr Leu Lys Gly Leu Gly Leu His Cys Pro Thr Tyr His Asn
127      290      295      300
128 Pro Ala Asp Phe Ile Ile Glu Val Ala Ser Gly Glu Tyr Gly Asp Leu
129 305      310      315      320
130 Asn Pro Met Leu Phe Arg Ala Val Gln Asn Gly Leu Cys Ala Met Ala
131      325      330      335
132 Glu Lys Lys Ser Ser Pro Glu Lys Asn Glu Val Pro Ala Pro Cys Pro
133      340      345      350
134 Pro Cys Pro Pro Glu Val Asp Pro Ile Glu Ser His Thr Phe Ala Thr
135      355      360      365
136 Ser Thr Leu Thr Gln Phe Cys Ile Leu Phe Lys Arg Thr Phe Leu Ser
137      370      375      380
138 Ile Leu Arg Asp Thr Val Leu Thr His Leu Arg Phe Met Ser His Val
139 385      390      395      400
140 Val Ile Gly Val Leu Ile Gly Leu Leu Tyr Leu His Ile Gly Asp Asp
141      405      410      415
142 Ala Ser Lys Val Phe Asn Asn Thr Gly Cys Leu Phe Phe Ser Met Leu
143      420      425      430
144 Phe Leu Met Phe Ala Ala Leu Met Pro Thr Val Leu Thr Phe Pro Leu
145      435      440      445
146 Glu Met Ala Val Phe Met Arg Glu His Leu Asn Tyr Trp Tyr Ser Leu
147      450      455      460
148 Lys Ala Tyr Tyr Leu Ala Lys Thr Met Ala Asp Val Pro Phe Gln Val
149 465      470      475      480
150 Val Cys Pro Val Val Tyr Cys Ser Ile Val Tyr Trp Met Thr Gly Gln
151      485      490      495
152 Pro Ala Glu Thr Ser Arg Phe Leu Leu Phe Ser Ala Leu Ala Thr Ala
153      500      505      510
154 Thr Ala Leu Val Ala Gln Ser Leu Gly Leu Leu Ile Gly Ala Ala Ser

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155          515          520          525
156 Asn Ser Leu Gln Val Ala Thr Phe Val Gly Pro Val Thr Ala Ile Pro
157          530          535          540
158 Val Leu Leu Phe Ser Gly Phe Phe Val Ser Phe Lys Thr Ile Pro Thr
159 545          550          555          560
160 Tyr Leu Gln Trp Ser Ser Tyr Leu Ser Tyr Val Arg Tyr Gly Phe Glu
161          565          570          575
162 Gly Val Ile Leu Thr Ile Tyr Gly Met Glu Arg Gly Asp Leu Thr Cys
163          580          585          590
164 Leu Glu Glu Arg Cys Pro Phe Arg Glu Pro Gln Ser Ile Leu Arg Ala
165          595          600          605
166 Leu Asp Val Glu Asp Ala Lys Leu Tyr Met Asp Phe Leu Val Leu Gly
167          610          615          620
168 Ile Phe Phe Leu Ala Leu Arg Leu Leu Ala Tyr Leu Val Leu Arg Tyr
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171          645
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 1941
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 3
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182 gagaaccaca tcaactgaagc ccagcgcttc tcccacctgc ccaagcgctc agccgtggac 180
183 atcgagttcg tggagctgtc ctattccgtg cgggaggggc cctgctggcg caaaaggggt 240
184 tataagacct ttctcaagtg cctctcaggt aaattctgcc gccgggagct gattggcatc 300
185 atggggccct caggggctgg caagtctaca ttcatgaaca tcttggcagg atacagggag 360
186 tctggaatga aggggcagat cctggttaat ggaaggccac gggagctgag gaccttccgc 420
187 aagatgtcct gctacatcat gcaagatgac atgctgctgc cgcacctcac ggtgttggaa 480
188 gccatgatgg tctctgctaa cctgaatctt actgagaatc ccgatgtgaa aaacgatctc 540
189 gtgacagaga tctgacggc actgggcctg atgtcgtgct cccacacgag gacagccctg 600
190 ctctctggcg ggcagaggaa gcgtctggcc atcgccctgg agctggtcaa caaccgcct 660
191 gtcattgttc ttgatgagcc caccagtggg ctggatagcg cctcttgttt ccaagtgggt 720
192 tccctcatga agtccttggc acaggggggc cgtaccatca tctgcacct ccaccagccc 780
193 agtgccaagc tctttgagat gtttgacaag ctctacatcc tgagccaggg tcagtgcata 840
194 ttcaaaggag tggtcaccaa cctgatcccc tatctaaagg gactcggctt gcattgcccc 900
195 acctaccaca acccgctga cttcatcatc gaggtggcct ctggcgagta tggagacctg 960
196 aaccccatgt tgttcagggc tgtgcagaat gggctgtgcg ctatggctga gaagaagagc 1020
197 agccctgaga agaacgaggt ccctgcccc tgcctcctt gtcctccgga agtggatccc 1080
198 attgaaagcc acaccttgc caccagcacc ctacacagc tctgcacct cttcaagagg 1140
199 accttctgt ccactctcag ggacacggtc ctgaccacc tacggttcat gtcccacgtg 1200
200 gttattggcg tgtcatcgg cctcctctac ctgcatattg gcgacgatgc cagcaagggtc 1260
201 ttcaacaaca ccggctgcct cttcttctcc atgctgttcc tcatgttcgc cgccctcatg 1320
202 ccaactgtgc tcaccttccc cttagagatg gcggtcttca tgagggagca cctcaactac 1380
203 tggtagagcc tcaaagcgtt ttacctggcc aagaccatgg ctgacgtgcc ctttcagggtg 1440
204 gtgtgtccgg tggctacttg cagcattgtg tactggatga cgggccagcc cgctgagacc 1500
205 agccgcttcc tgctcttctc agccctggcc accgccaccg ccttgggtggc ccaatctttg 1560
206 gggctgctga tcggagctgc ttccaaactcc ctacagtggt ccacttttgt gggccagtt 1620

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207 accgccatcc ctgtcctctt gttctccggc ttctttgtca gcttcaagac catccccact 1680
208 tacctgcaat ggagtccta tctctcctat gtcaggatg gctttgaggg tgtgatactg 1740
209 acgatctatg gcatggagcg aggagacctg acatgttttag aggaacgctg cccgttccgg 1800
210 gagccacaga gcatcctccg agcgctggat gtggaggatg ccaagctcta catggacttc 1860
211 ctggtcttgg gcatcttctt cctagccctg cggtctctgg cctaccttgt gctgcgttac 1920
212 cgggtcaagt cagagagata g 1941
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 674
216 <212> TYPE: PRT
217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 4
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221 1 5 10 15
222 Ala Glu Met Thr Glu Pro Lys Ser Val Cys Val Ser Val Asp Glu Val
223 20 25 30
224 Val Ser Ser Asn Met Glu Ala Thr Glu Thr Asp Leu Leu Asn Gly His
225 35 40 45
226 Leu Lys Lys Val Asp Asn Asn Leu Thr Glu Ala Gln Arg Phe Ser Ser
227 50 55 60
228 Leu Pro Arg Arg Ala Ala Val Asn Ile Glu Phe Arg Asp Leu Ser Tyr
229 65 70 75 80
230 Ser Val Pro Glu Gly Pro Trp Trp Arg Lys Lys Gly Tyr Lys Thr Leu
231 85 90 95
232 Leu Lys Gly Ile Ser Gly Lys Phe Asn Ser Gly Glu Leu Val Ala Ile
233 100 105 110
234 Met Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Met Asn Ile Leu Ala
235 115 120 125
236 Gly Tyr Arg Glu Thr Gly Met Lys Gly Ala Val Leu Ile Asn Gly Leu
237 130 135 140
238 Pro Arg Asp Leu Arg Cys Phe Arg Lys Val Ser Cys Tyr Ile Met Gln
239 145 150 155 160
240 Asp Asp Met Leu Leu Pro His Leu Thr Val Gln Glu Ala Met Met Val
241 165 170 175
242 Ser Ala His Leu Lys Leu Gln Glu Lys Asp Glu Gly Arg Arg Glu Met
243 180 185 190
244 Val Lys Glu Ile Leu Thr Ala Leu Gly Leu Leu Ser Cys Ala Asn Thr
245 195 200 205
246 Arg Thr Gly Ser Leu Ser Gly Gly Gln Arg Lys Arg Leu Ala Ile Ala
247 210 215 220
248 Leu Glu Leu Val Asn Asn Pro Pro Val Met Phe Phe Asp Glu Pro Thr
249 225 230 235 240
250 Ser Gly Leu Asp Ser Ala Ser Cys Phe Gln Val Val Ser Leu Met Lys
251 245 250 255
252 Gly Leu Ala Gln Gly Gly Arg Ser Ile Ile Cys Thr Ile His Gln Pro
253 260 265 270
254 Ser Ala Lys Leu Phe Glu Leu Phe Asp Gln Leu Tyr Val Leu Ser Gln
255 275 280 285
256 Gly Gln Cys Val Tyr Arg Gly Lys Val Cys Asn Leu Val Pro Tyr Leu
257 290 295 300

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→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/090,455

DATE: 03/19/2002

TIME: 15:56:15

Input Set : A:\406.app

Output Set: N:\CRF3\03192002\J090455.raw

L:12 M:270 C: Current Application Number differs, Wrong Format

L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13